

Fig. 1A

The image shows a gel electrophoresis result with four lanes labeled at the top: **Translat/fusion**, **Oligo-dT**, **Ni-NTA**, and **RT**. On the right side, five arrows point to specific bands, labeled from top to bottom: **well**, **mRNA-pep**, **RT'ed mRNA-pep**, **NS**, and **free pep**. The **Translat/fusion** lane shows a very dark, thick band at the **well** position. The **Oligo-dT** lane shows a band at the **mRNA-pep** position. The **Ni-NTA** lane shows a band at the **mRNA-pep** position. The **RT** lane shows a band at the **RT'ed mRNA-pep** position.

Fig. 1B

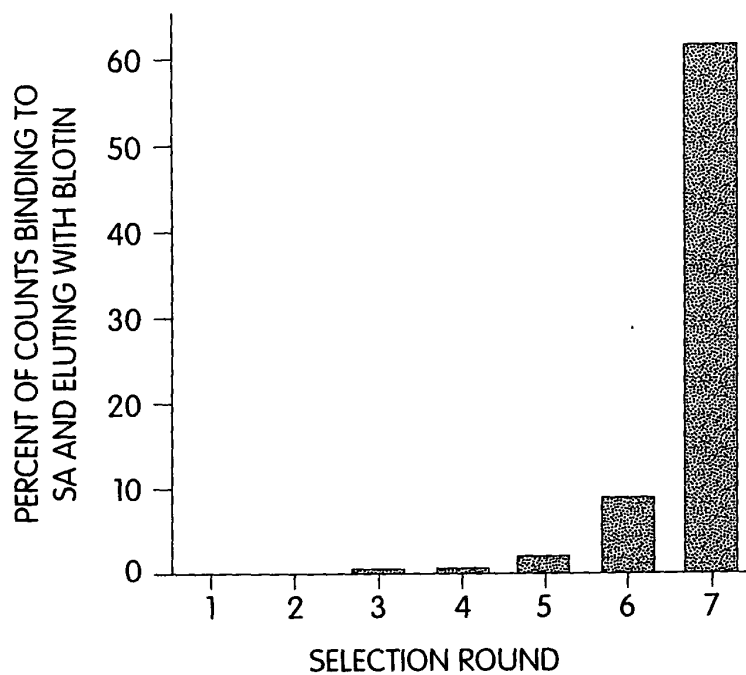


Fig. 2A

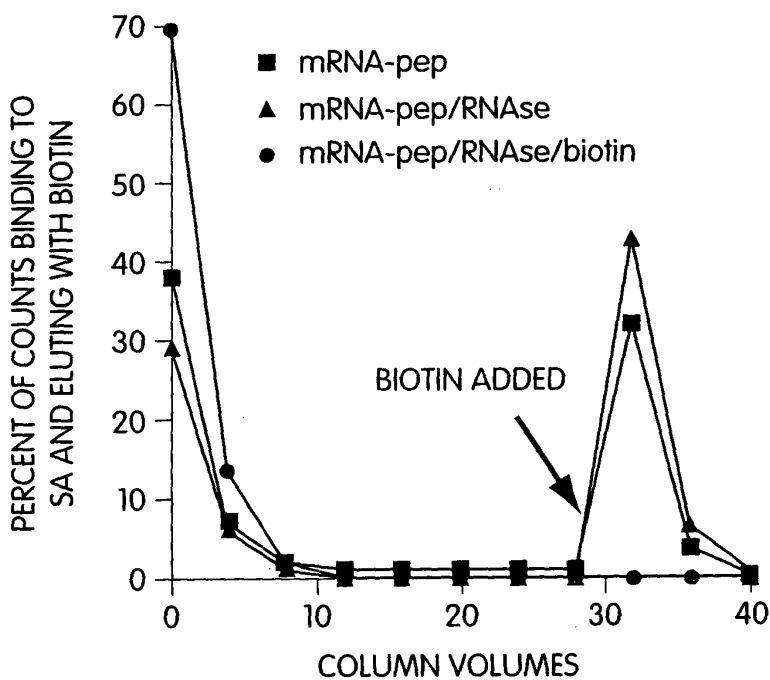


Fig. 2B

Figure 3

name #	SEQ	ID NO:
SB1 3	<u>MDEKTHCTIS</u> MNGAVPLVPHH HPQ QDPLURLLHRPQAPALLVR HPQ QDLVALVEHHEGVDRGLVALPELHAEEIGEPVGDVQGPVEQVQGVVDALVWRLPPS	1
SB2 2	<u>MDEKTHCFHPG</u> DHLVRLVEELQALAEGLQRQGGRRQPHRLPRRRPHHLQLLLDEA HPQ AGPLRERAHQVDGRILLQL HPQ GGDRLLQQPQDPHLELVWRLPPS	2
SB3 4	<u>MTRRP</u> TASSSSCVRHLLLRQGEHGHQALEDRDKARHVRLVEGDVEVLGGDLRLARARHEAL HPQ AGLVHLPLHGGDLGGHLRLVLEA HPQ QDRGLGLAVHHH	3
SB4 1	<u>MDEKTHWGI</u> STWRGEPDLL HPQ AGRLPLDRRRARHRRILGAEPGGVDHGLRLELLDDHRPLVPD HPQ RGPLQRGDLPQVVPVLRLRHAHVGLGLGLAAATIT	4
SB5 3	<u>MDEKTHWNVVY</u> HPQ QDILLVRGHGHDVEALHDQGLHQLDLLVGPPEVVRALRGEVLGGRLRLVPLD HPQ QGEALDQARQRPQHLLLELHHRALPPALVWRLPPS	5
SB6 1	<u>MDEKTHLNN</u> FEELLARLDGLREGEDHPLVLR HPQ QDGLLDQPLGRHRALDGEVREGDRPLDQGGGEEDLGALVDDDDGEVLDGLVHVGVHVDPLVCGCHHH	6
SB7 1	<u>MDEKTHWFG</u> TLNSFPTHMMSAVGNKIDCSFNMNLSLNHWLSSGHPDGDALDDQ HPQ GDALVGRDDGVQALRLEGHQHRRLLAQRRAADRHRQLVWRLPPS	7
SB8 1	<u>MDEKTHCTI</u> ELNFSFTHWKLHH HPQ QGDALLDDGVRPHHPLADEGGGLDDQGLGHRRGVVAERLARRDPEVLEGLVERHRGLVPRLRHGGGERHAEPVWRLPPS	8
SB9 1	<u>MDEKTHCNT</u> GLYDGAADCFNELNKDVAFLVEGRHDLVEGLLLER HPQ QDPLVAHRQLVHHPLLGGERHRRALVPQQEHQPHRLQPVVDLGRRRLVWRLPPS	9
SB10 1	<u>MDEKTHWHERA</u> QELVGGLLLHD HPQ RLLEPRGPRPLRGLVHERGHQPQPLAGRVEEADGGLLRDGGGELEPLVREGEDHLEPLDDELDAGRGLVWRLPHHH	10
SB11 1	<u>MDEKTHWHERV</u> HHLADGLE HPQ QQRRLVERHRQVPRGLVRELQHEGLPLEHPAGVHVIRLHQGDDRDVDGLVDGCHGRDVRGLEREVEVGDPHRLVWRLPPS	11
SB12 4	<u>MDKDP</u> LLELEELRERLV HPQ QGLLPLRGQVGHDAERLGAEVDDLRGGLLDEPQRAVAGLHHVPHRVGQRLVHEVRELDGLDDQRDDLRQLVWRLPPS	12
SB13 2	<u>MERED</u> PLDEQLRELREALVD HPQ QGAQALHRHDGGEHVPLRRVQHRLQPGLQHLELPQPLGELQARLQPLAGEHEGDCAGLQRPVPGHQGRRLVWRLPPS	13
SB14 1	<u>MDEKTHRT</u> LSVLSFNDFMLGQTKACWRLVEGLH HPQ QGLVREHEVDVLPLAEVQVQVVGGLADGVEQPGGGLLHRAQRVDHPLPDHAGQVLGRVWRLPPS	14
SB15 1	<u>MDEKTHWLED</u> LKGVLDCLKDLMDFTKDCRSPRVQPOPLLHHDGRGEPVPLLRACGRDLGGLGPRAPRQARPLHHGRHDLHEPLVLQD HPQ GGPLVCGCHHH	15
SB16 1	<u>MDEKTHWVL</u> QL HPQ QDRLGPRHGGDDVRLVGQGEVLEGLDGRPRRRRHRLPREDEHRVRLVDQVRDLAERLVEEVGQVEALRHLGLPQDEPRSGGCHHH	16
SB17 2	<u>MDEKTHWVG</u> DLQEPPLGPHGGVGEVPGGLVLR HPQ QRDLNDGVGPHGRALARRRPHRWEGHLHLLQRGGERLPPDGPRQLGLLGGELDRADPALVWRLPPS	17
SB18 1	<u>MDEKTHCAV</u> NVNVGLTHWCHRVAHLQPLD HPQ GDHLRLEPLGHALVDPLVQGVVEVVRPLQLDVGVRVALVEQVAEVGEGLDHEAGQAHGALVWRLPPS	18
SB19 1	<u>MDEKTTG</u> WRGGHVVEGLAGELEQLRARLE HPQ QGREPLVQVEEDVEGLVQDLHGVAAGLLDPVEKLLTDMFKFKFNVSCKDKMTFYLEMVDWSGGCHHH	19
SB20 1	<u>MNEKTHCK</u> LNFKVNIADWLAEFFHGGGGLLRDDGVVQRLVDGVQERVERLDRDPGLGDLRLLELHRDRLRUGGEHLRDLRHPLEPDDHLVVGGLVWRLPPS	20

Fig. 3

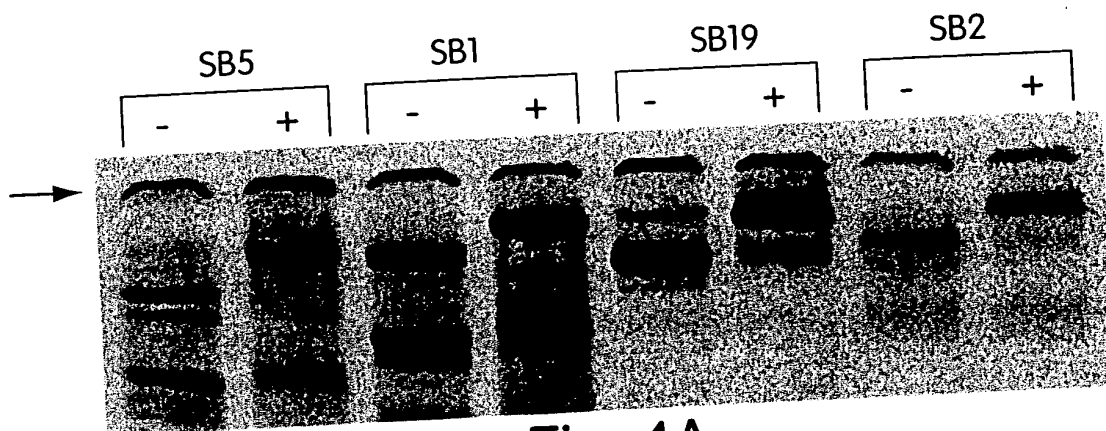


Fig. 4A

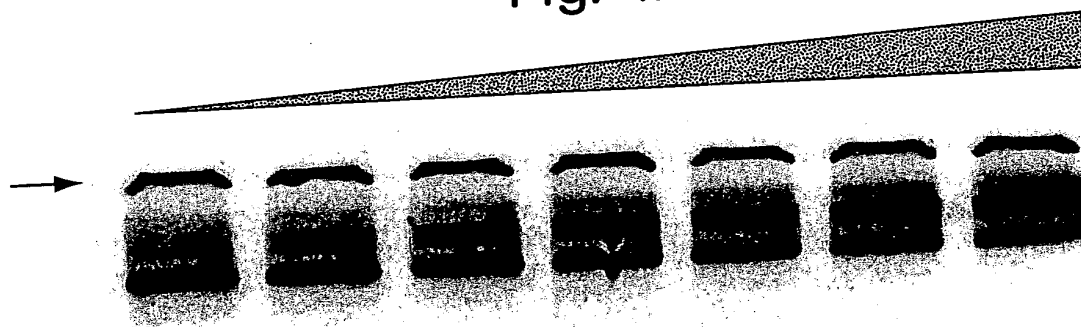


Fig. 4B

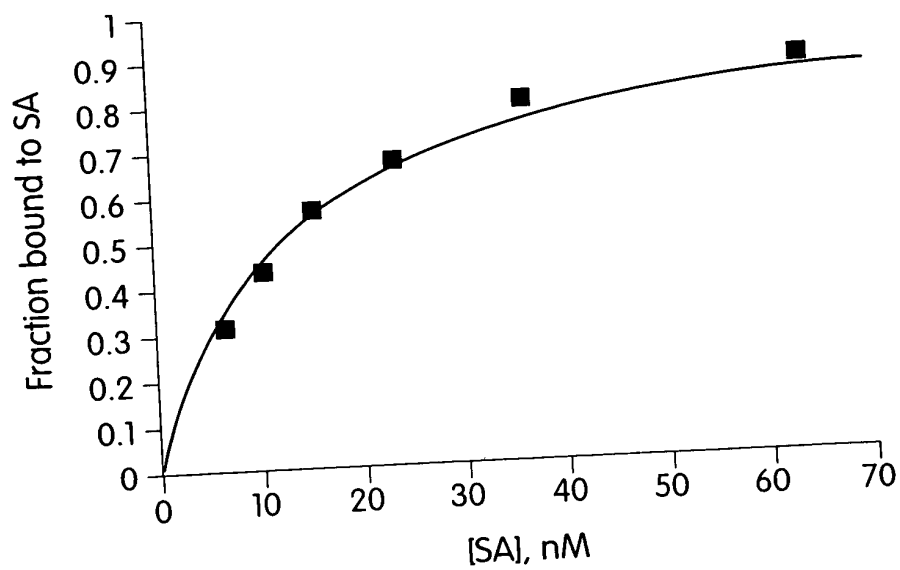


Fig. 4C

Foot "Foot"

		% binding	SEQ ID NO:
FL	MDEKTTGWRGCHVVEGLAGELEQLRARLEHHPQGQREPLVQVEEDVDEGLVQDLHGVAAGLLDPVEKLLTDWFKKFKNVSKDCRMTFFYLEMYDWSGGCKLG	85	21
C1	MDEKTTGWRGCHVVEGLAGELEQLRARLEHHPQGQREPLVQVEEDVDEGLVQDLHGVAAGLLDPVEKLLTDWFKKFKNV	87	22
C2	MDEKTTGWRGCHVVEGLAGELEQLRARLEHHPQGQREPLVQVEEDVDEGLVQDLHGVAAGLLDPVE	88	23
C3	MDEKTTGWRGCHVVEGLAGELEQLRARLEHHPQGQREPLVQVEEDVDEGLVQDLHGVAAGLLDPVE	89	24
C4	MDEKTTGWRGCHVVEGLAGELEQLRARLEHHPQGQREPLVQVEEDVDEGLVQ	88	25
M1	MDEKTTGWRGCHVVEGLAGELEQLRARLEHHPQGQREPLVQVEEDVDEGLVQ	0.065	26
N1	MD	69	27
N2	MD	30	28
N3	M	0.058	29

Fig. 5

Fig. 6A

CGCAAAATTGTCGGCGCGATTAAATCTCGCGCCGATCAACTGGTGCCAGCGTGGTGTGTCGATGGTAGAACGACGGGC
 GTCGAAGCCTGTAAAGCGCGGTGCACAAATCTTCTCGGCAACGCGTCAGTGGGTGATCATTAACATATCCGCTGGATGA
 CCAGGATGCCATTGCTGTGGAAGCTGCCGTGCACATAATGTTCCGGCGTTATTCTTGATGTCTCTGACGACGACCCCATCA
 ACAGTATTATTTTCTCCCATGAAGACGGTACCGGACTGGCGGTGAGCATCTGGTCGCATTGGTCACGACAAATCGCG
 CTGTTAGCGGGCCCATTAAGTTCTGTCTCGGGCGCTGCGTCTGGCTGGCATAAATATCTCACTCGCAATCAAAAT
 TCAGCCGATAGCGGAACGGGAAGGCGACTGGAGTGCCATGTCCGGTTTTCAACAAACCATGCAAAATGCTGAATGAGGGCA
 TCGTTCACCATGCGATGCTGGTTGCCAACGATCAGATGGCGTGGGCGCAATGCGGCCATTACCGAGTCCGGGCTGCGC
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 GATTCATTAAATGCACTGGCAGCAGAGGTTTCCCGACTGGAAGCGGCGAGTGAGCGCAACGCAATTAATGTAAGTTAGC
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 GTGTTTCGTAAAGTCTGGAACCGCGAAGTCAGGCCCCGACCATATGTTCCGGATCTGCATCGCAGGATGCTGTGG
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 CCATACCGCCAGTTGTTTACCCTCACAAAGTTCCAGTAACCGGCGATGTTCAATCATAGTAACCCGTATCGTGAGCATCC
 TCTCTCGTTTCATCGGTATCATTAACCCCATGAACAGAAATCCCCCTTACGAGGCGATCAGTGACCAACAGGAAAAA
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 ACAGGCAGACATCTGTGAATCGCTTACGACCCACGCTGATGAGCTTTACCGAGCTGCCCTCGCGCTTTCGGTGTGACG
 GTGAAAACCTCTGACACATGCACTCCCGGAGACGGTCACAGCTTGCTGTAAAGCGGATGCCGGAGCAGACAAAGCCCGT
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 AGAAAATACCGCATCAGGCGCTCTTCGCTTCTCGCTCACTGCTCGCTGCGCTCGGTGCTGCTCGGCTCGGCGAGCGGT
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 AATCGACGCTCAAGTCAGAGGTGGCGAAACCCGACAGGACTATAAGATACAGGCGTTTCCCCCTGGAAGCTCCCCCTCGT
 GCGCTCTCCTGTTCCGACCCCTGCCGCTTACCGGATACCTGTCCGCGCTTCTCCCTTCGGGAAGCGTGGCGCTTCTCTCATA

Fig. 6A (continued)

Fig. 6A

GCTCAGCGTGTAGGTATCTCAGTTCGGTGTAGTCTCGTTCGCTCCAAGCTGGGCTGTGTGCACGAACCCCCCGTTTCAGCCC
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 GAGGTGCCGTAAAGCACTAAATCGGAACCCCTAAAGGAGCCCCCGATTAGAGCTTGACGGGGAAGCCGGCAACGTGG
 CGAGAAAGGAAGGAAGCAAGGAGCGGCGCTAGGGCGCTGGCAAGTGTAGCGGTCAACGCTGCGCGTAAACCA
 ACACCCGCGCGCTTAATGCGCCCGCTACAGGGCGCGTCCCATTCGCCA

Fig. 6A (continued)

(SEQ ID No.:38)

MGIEGKLVINGDKGYNGLAEVGKKFEKDTGIKVTVEHPDKLEEKFPQVAATGDGPDIIFWAHDRFGGYAQSGLLAEI
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LIAADGGYAFKYENGKYDIKDVGVNDNAGAKAGLTFLVDLIKKNHNMNADTDYSIAEAAFNKGETAMTINGPWAWNSNIDTSK
VNYGVTVLPTFKGQPSKPFVGVLSAGINAASPNKELAKEFLENYLLTDEGLEAVNKDKPLGAVALKSYEEELAKDPRIAA
TMENAQKGEIMPNI PQMSAFWYAVRTAVINAASGRQTVDEALKDAQTNSSSGSGSGSGMDEKTTGWRGGHVVEGLAGELEQ
LRARLEHHFPQGQREP GSGHHHHHHHEFLVPRGSMDDPCVKCKVAPRNWKVKNKHLRIYNMCKTCFNNSIDIGDDTYHGHDD

Fig. 6B

(SEQ ID No.:39)

MDPCVKCKVAPRNWKVKNKHLRIYNMCKTCFNNSIDIGDDTYHGHDD

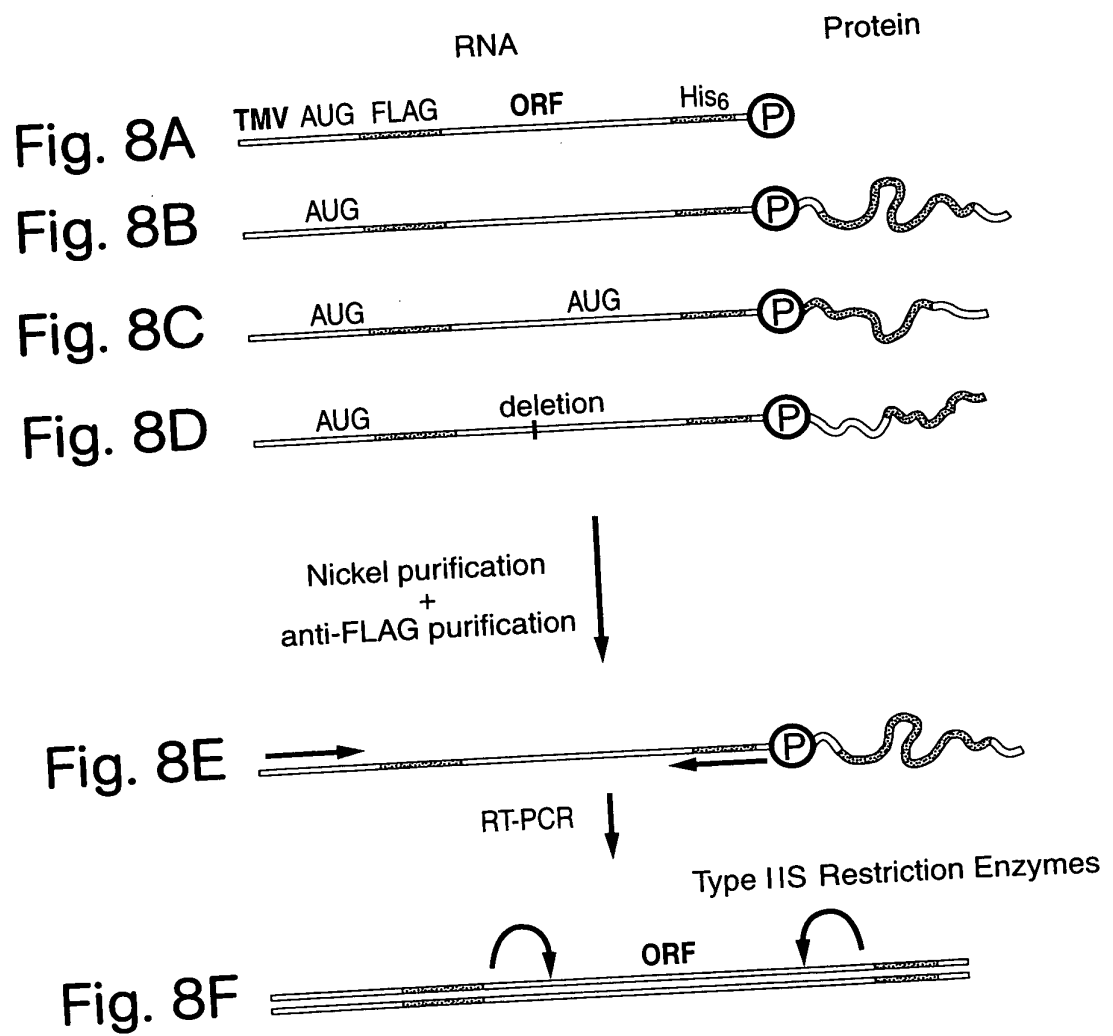
Fig. 6C

Abstract

Fig. 7A



Fig. 7B



ACTATCCGCTGGATGACCAGGATGCCATTGCTGTGGAAGCTGCCCTGCACTAAATGTTCCGGCGTTATTCTTGATGTCTCT
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CGAGTCCGGGCTGCGGCTGTGCGGATATCTCGGTAGTGGGATACGACGATACCGAAGACAGCTCATGTTATATCCCGC
CGTTAACCAACCATCAACAGGATTTTCCCGTCTCACTGGTGAAAGAAACCAACCCCTGGCGCCCAATACGCAAAACCGCCTC
GCGGTGAAGGGCAATCAGCTGTTGCCGCTCACTGGTGAAAGAAACCAACCCCTGGCGCCCAATACGCAAAACCGCCTC
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CCGGTGGGCGGGGGCATGACTATCGTGGCGCACTTATGACTGTCTTATCATGCAACTCGTAGGACAGGTGCCGG
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CATGGCGGCCACGGGTGCGCATGATCGTCTCTGTGCTGAGGACCCGGTAGGCTGGCGGGGTTGCCCTTACTGGTT
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ATGGTCTTCGGTTCCGTGTTTCGTAAGTCTGAAACCGGGAGTCAAGCCCTGCAACCATTATGTTCCGGATCTGCAT
CGCAGGATGCTGCTGGCTACCTGTGGAACACCTACATCTGTATTAACGAAGCGTGGCATTGACCCGTGAGTGATTTTC
TCTGGTCCCGCGCATCCATACCGCCAGTTGTTACCTCACAACGTTCCAGTAACCGGGCATGTTTCATCATCAGTAACC
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Fig. 9A (continued)

Sequence

CACTGGCAGCAGCCACTGGTAACAGGATTAGCAGAGCGAGGTATGTAGGCGGTGCTACAGAGTTCTTGAAGTGGTGGCCT
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 CTAGGCCGCGATTAAATCCCAACATGGATGCTGATTTATATGGGTATAAATGGCTCGCGATAATGTCGGCAATCAGGT
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 GATTTCTCACTGATAACCTTATTTTGACGAGGGAAATTAATAGTTGTTATGATGTTGGACGAGTCGGAATCGCAGA
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 CGGATACATATTTGAATGTATTTAGAAAAATAAACAATAGGGTTCCGCGCACATTTCCCCGAAAAAGTGCCACCTGAAA
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 GGCAAAATCCCTTATAAATCAAAAGAAATAGACCGAGATAGGGTTGAGTGTGTTCCAGTTTGGAAACAAGATCCCACTATT
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 CAAGTTTTTTGGGTCGAGGTGCCGTAAGCACTAAATCGGAACCCCTAAAGGGAGCCCCCGATTAGAGCTTGACGGGA
 AAGCCGGCGAACGTGGCGAGAAAGGAAGGAAAGCAAGGAGCGGGCGCTAGGGCGCTGGCAAGTGTAGCGGTAC
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Fig. 9A (continued)

[illegible]

(SEQ ID No.: 41)

MGIEEGKLIWINGDKYNGLAEVGKKFEKDTGIKVTVEHPDKLEEKFPQVAATGDGPDIIFWAHDRFGGYAQSGLLAEI
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LIAADGGYAFKYENCKYDIKDVGVDNAGAKAGLTFVLVDLIKKNHMNADTDYSIAEAAFNKGETAMTINGPWAWSNIDTSK
VNYGTVLPTFKGQPSKPFVGVLSAGINAA SPNKELAKEFLENYLLTDEGLEAVNKDKPLGAVALKSYEEELAKDPRIAA
TMENAQKGEIMPNIPQMSAFWYAVRTAVINAA SGRQTVD EAL KDAQTNSSSGSGSGMDEKTTGWRGGHVVEGLAGELEQ
LRARLEHHPPQGPQREP GSGHHHHHHHEF

Fig. 9B

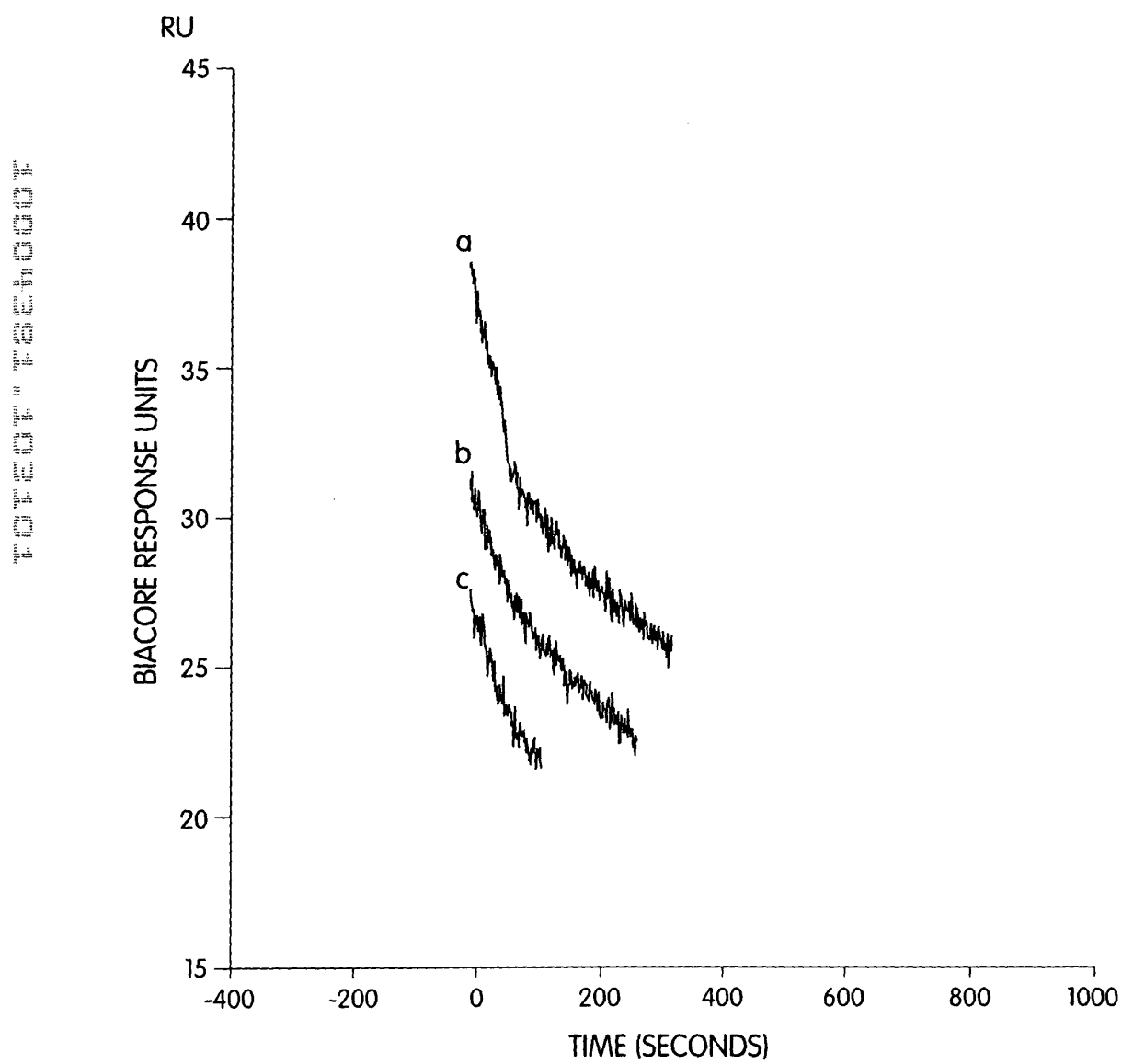


Fig. 10A

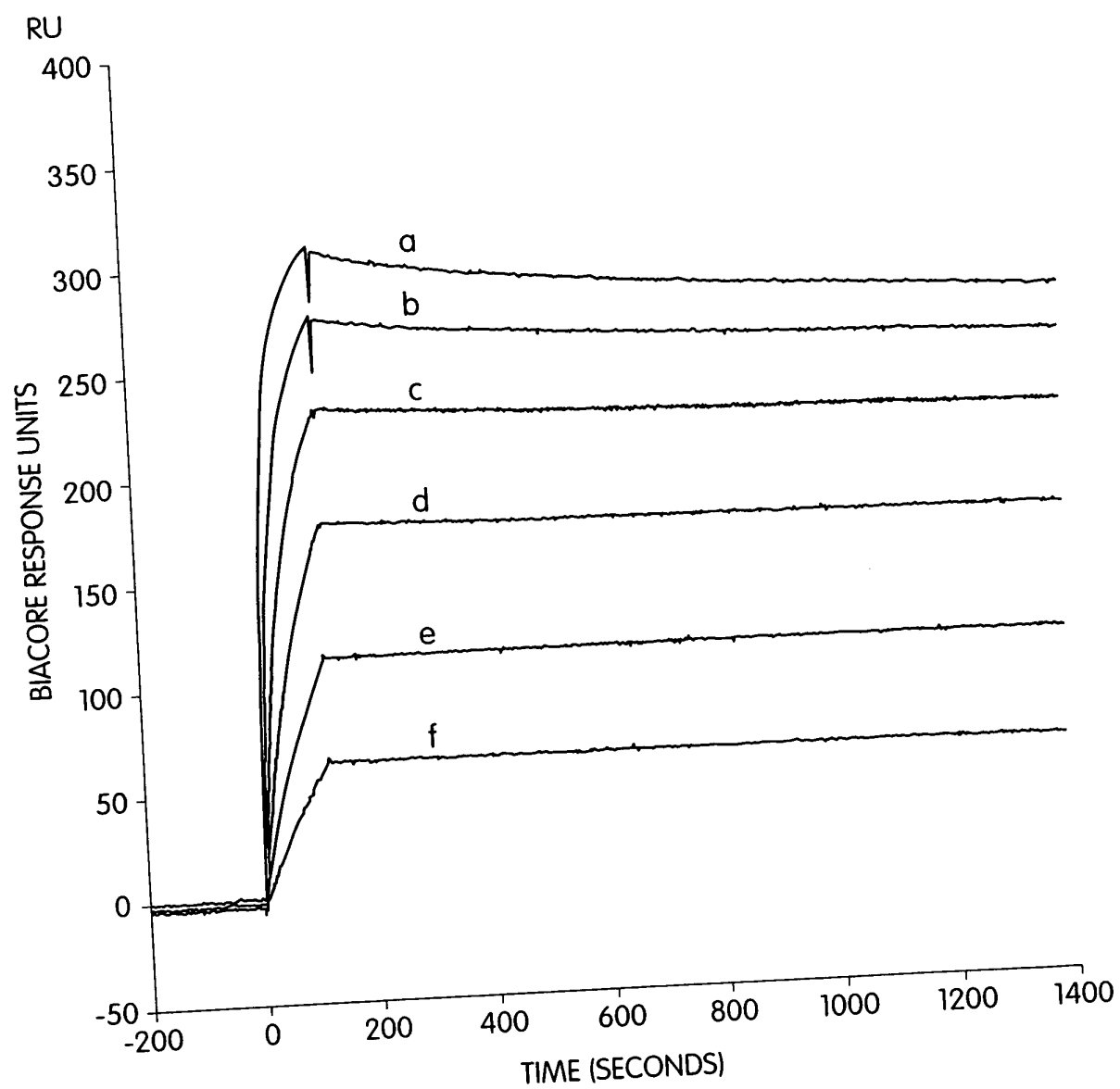


Fig. 10B

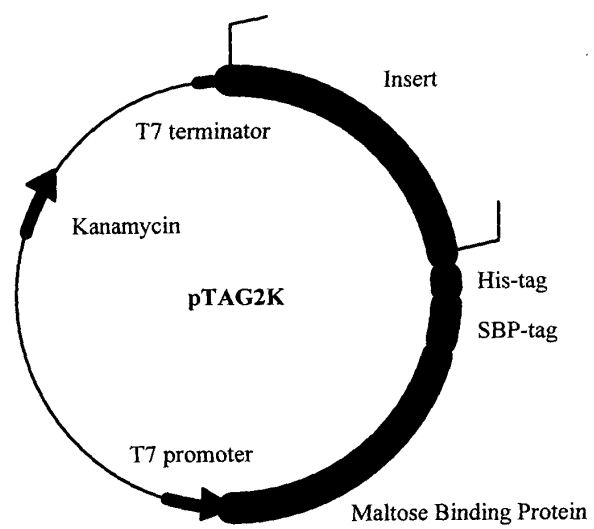


Fig. 11

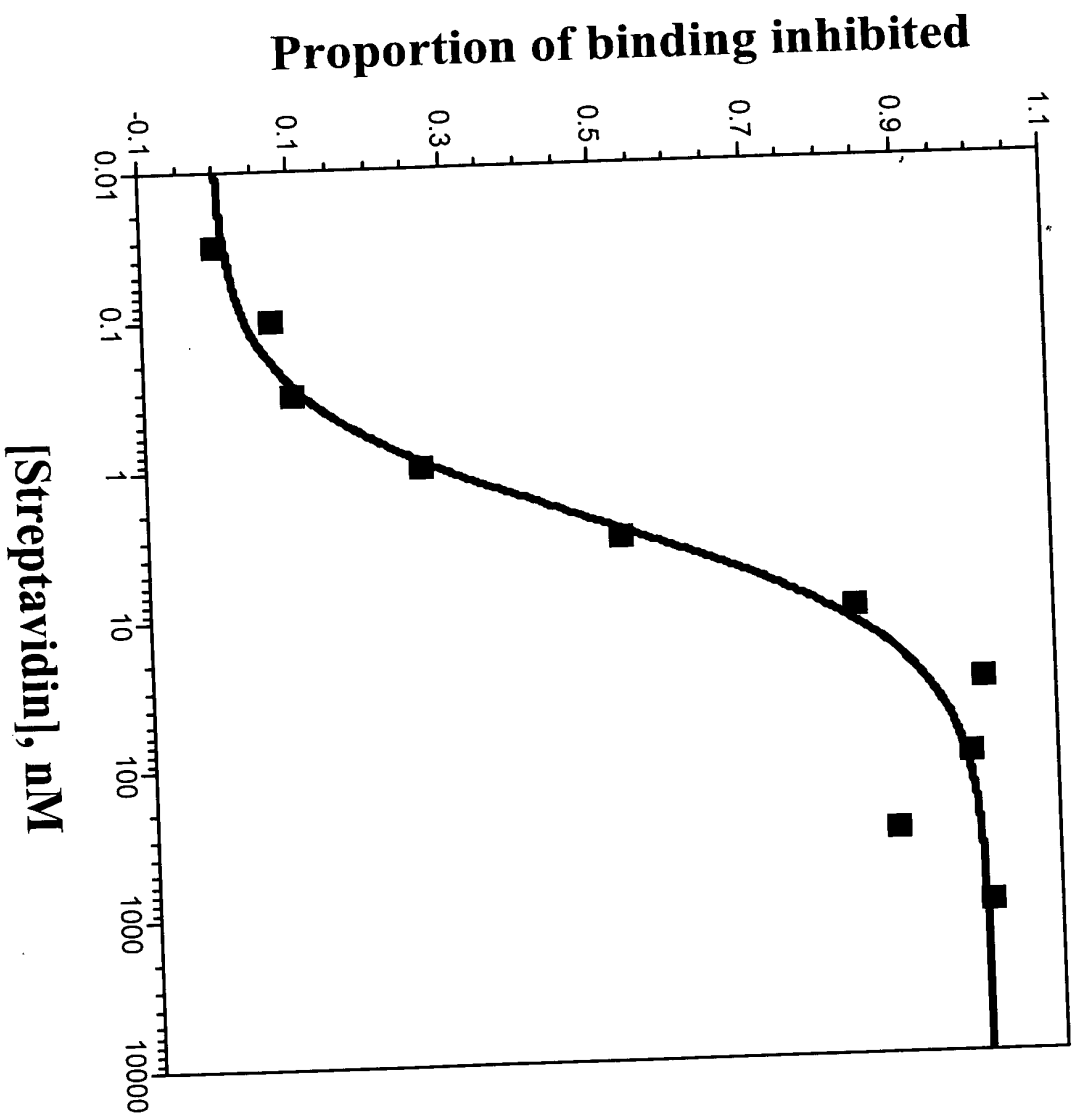


Fig. 12

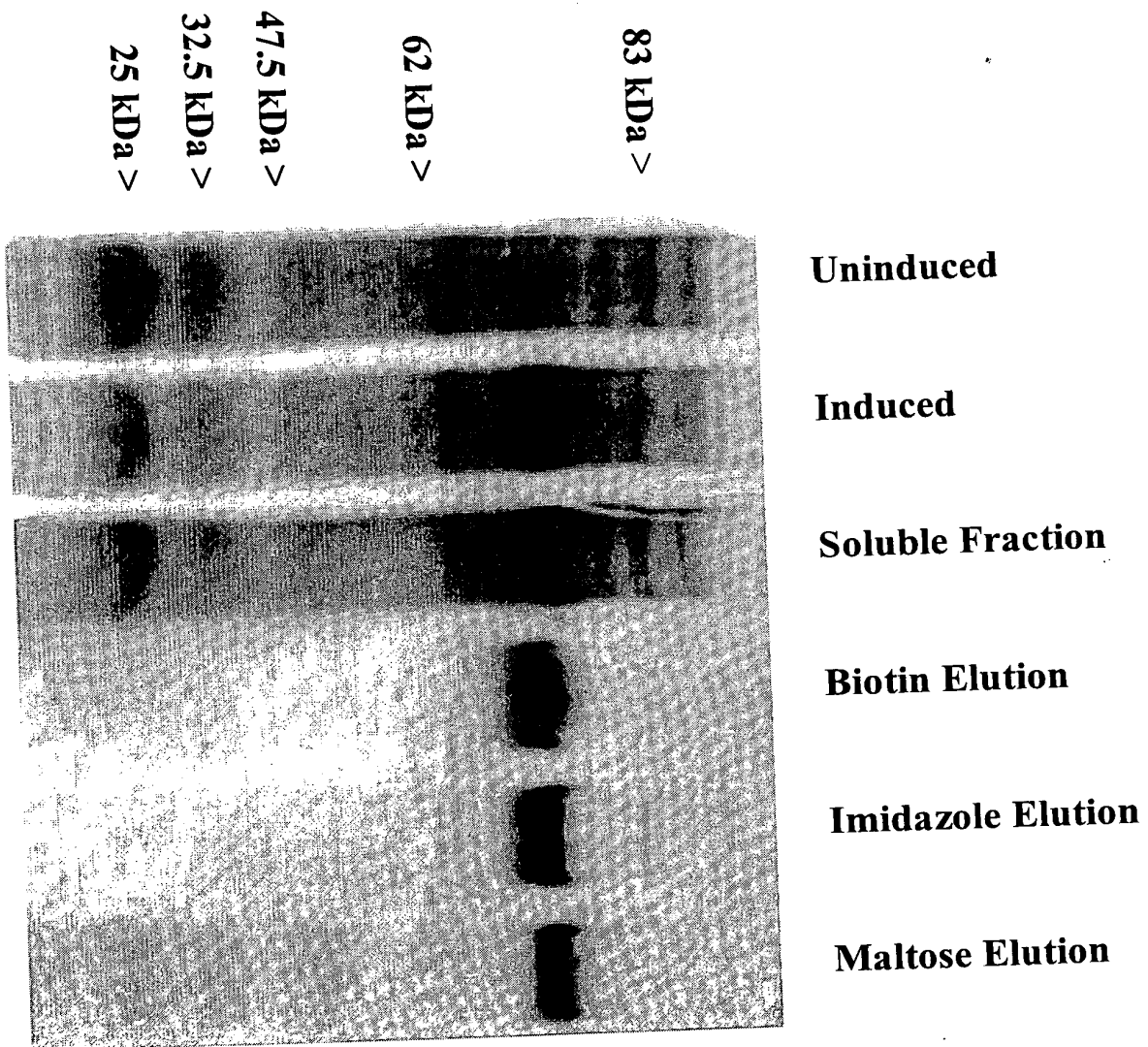


Fig. 13

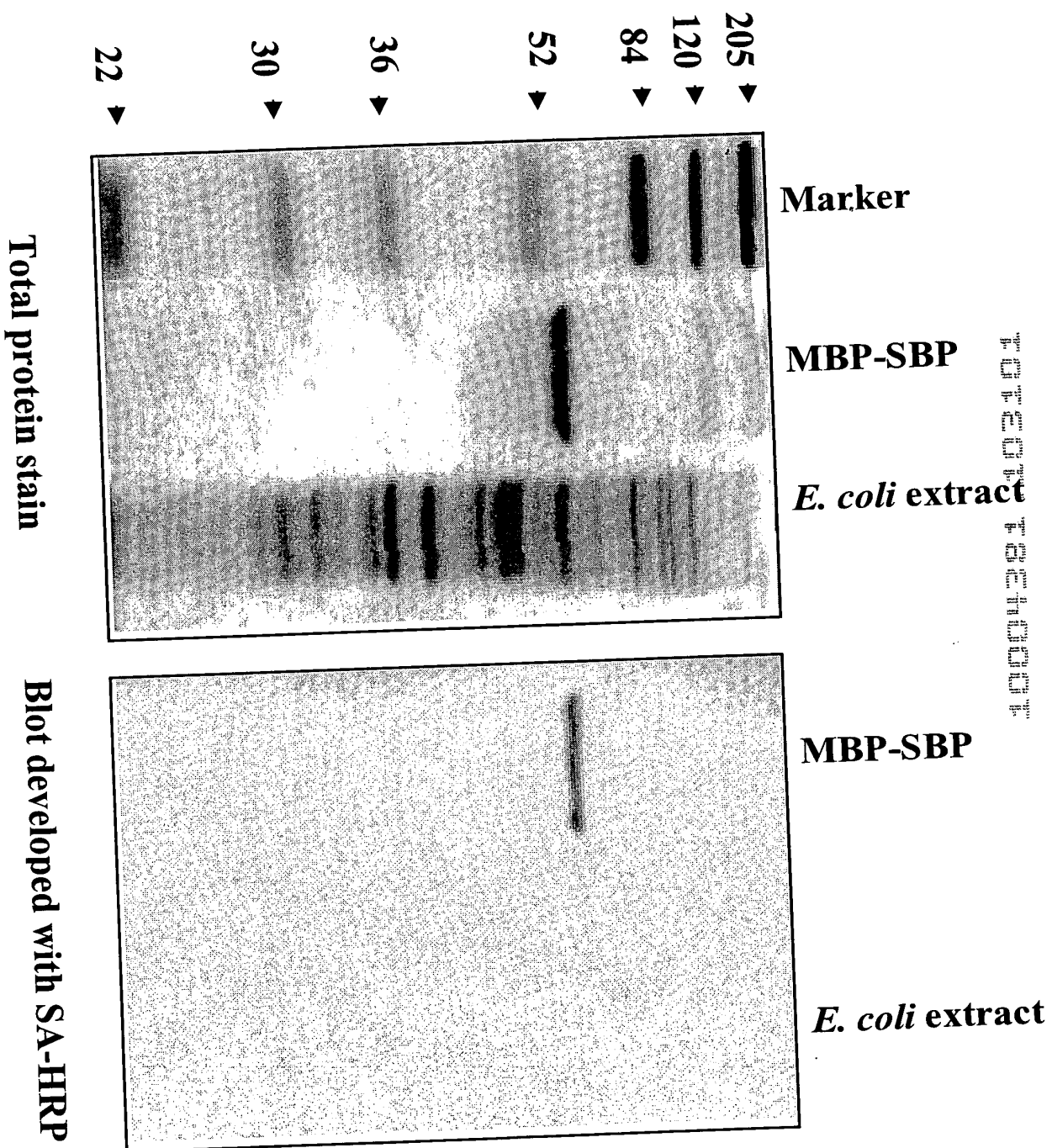


Fig. 14

Figure 1 is a graph showing the fraction of binding inhibited versus the concentration of SA (nM) on a semi-logarithmic scale. The x-axis is labeled "[SA], nM" and ranges from 0.001 to 100,000 on a log scale. The y-axis is labeled "Fraction binding inhibited" and ranges from -0.2 to 1.2. The data points (squares) show a sigmoidal curve that plateaus at a fraction of 1.0. A solid line represents the best fit to the data.

[SA], nM	Fraction binding inhibited
0.01	0.06
0.03	0.03
0.1	0.02
0.3	0.04
1	0.28
3	0.63
10	0.82
30	0.94
100	0.89
300	0.93
1000	1.04
3000	1.08
10000	1.11

Fig. 15